1 tgagggcgcc **atg**aggagcc tgtgctgcgc cccactcctg ctcctcttgc tgctgccgcc
61 gctgctgctc acgccccgcg ctggggacgc cgccgtgatc accggggctt gtgacaagga
121 ctcccaatgt ggtggaggca tgtgctgtgc tgtcagtatc tgggtcaaga gcataaggat
181 ttgcacacct atgggcaaac tgggagacag ctgccatcca ctgactcgta aaaacaattt
241 tggaaatgga aggcaggaaa gaagaaagag gaagagaagc aaaaggaaaa aggaggttcc
301 atttttggg cggaggatgc atcacacttg cccatgtctg ccaggcttgg cctgtttacg
361 gacttcattt aaccgattta tttgtttagc ccaaaag**taa** tcgctctgga gtagaaacca
421 aatgtga

FIGURE 1

MRSLCCAPLLLLLLLPPLLLTPRAGDAAVITGACDKDSQCGGGMCCAVSIWVKSIRICT
PMGKLGDSCHPLTRKNNFGNGRQERRKRKRSKRKKEVPFFGRRMHHTCPCLPGLACLRT
SFNRFICLAQK

FIGURE 2

1 tgagggcgcc **atg**aggagcc tgtgctgcgc cccactcctg ctcctcttgc tgctgccgcc
61 gagggcgcca tgaggagcct gtgctgcgcc ccactcctgc tcctcttgct gctgccgccg
121 ctgctgctca cgccccgcgc tggggacgcc gccgtgatca ccggggcttg tgacaaggac
181 tcccaatgtg gtggaggcat gtgctgtgct gtcagtatct gggtcaagag cataaggatt
241 tgcacaccta tgggcaaact gggagacagc tgccatccac tgactcgtaa agttccattt
301 tttgggcgga ggatgcatca cacttgccca tgtctgccag gcttggcctg tttacggact
361 tcatttaacc gatttatttg tttagcccaa aag**taa**tcgc tctggagtag aaaccaaatg
421 tga

FIGURE 3

MRSLCCAPLLLLLLPPLLLTPRAGDAAVITGACDKDSQCGGGMCCAVSIWVKSIRICT
PMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLACLRTSFNRFICLAQK

FIGURE 4

```
1     cggacgcgtg ggcgtcccct aaccgccacc gcgtccccgg gacgccatgg gggacccgcg
61    ctgtgccccg ctactgctac ttctgctgct accgctgctg ttcacaccgc ccgccgggga
121   tgccgcggtc atcaccgggg cttgcgacaa ggactctcag tgcggaggag gcatgtgctg
181   tgctgtcagt atctgggtta agagcataag gatctgcaca cctatgggcc aagtgggcga
241   cagctgccac cccctgactc ggaaagttcc attttggggg cggaggatgc accacacctg
301   cccctgcctg ccaggcttgg cgtgtttaag gacttctttc aaccggttta tttgcttggc
361   ccggaaatga tcactctgaa gtaggaactt gaaatgcgac cctccgctgc acaatgtccg
421   tcgagtctca cttgtaattg tggcaaacaa agaatactcc agaaagaaat gttctccccc
481   ttccttgact ttccaagtaa cgtttctatc tttgattttt gaagtggctt tttttttttt
541   ttttttttcc tttccttgaa ggaaagtttt gatttttgga gagatttata gaggactttc
601   tgacatggct tctcatttcc ctgtttatgt tttgccttga cattttgaa tgccaataac
661   aactgttttc acaaatagga gaataagagg gaacaatctg ttgcagaaac ttccttttgc
721   cctttgcccc actcgccccg ccccgccccg ccccgccctg cccatgcgca gacagacaca
781   cccttactct tcaaagactc tgatgatcct caccttactg tagcattgtg ggtttctaca
841   cttccccgcc ttgctggtgg acccactgag gaggctcaga gagctagcac tgtacaggtt
901   tgaaccagat cccccaagca gctcatttgg ggcagacgtt gggagcgctc caggaacttt
961   cctgcaccca tctggcccac tggctttcag ttctgctgtt taactggtgg gaggacaaaa
1021  ttaacgggac cctgaaggaa cctggcccgt ttatctagat ttgtttaagt aaaagacatt
1081  ttctccttgt tgtggaatat tacatgtctt tttctttttt atctgaagct tttttttttt
1141  ttctttaagt cttcttgttg gagacatttt aaagaacgcc actcgaggaa gcattgattt
1201  tcatytggca tgacaggagt catcatttta aaaaatcggt gttaagttat aatttaaact
1261  ttatttgtaa cccaaaggty taatgtaaat ggatttcctg atatcctgcc atttgtactg
1321  gtatcaatat ttytatgt
```

FIGURE 5

MGDPRCAPLLLLLLPLLFTPPAGDAAVITGACDKDSQCGGGMCCAVSIWVKSIRICTP
MGQVGDSCHPLTRKVPFWGRRMHHTCPCLPGLACLRTSFNRFICLARK

FIGURE 6

```
                10        20        30        40        50
Human BV8       MRSLCCAPLLLLLLPPLLLTPRAGDAAVITGACDKDSQCGGGMCCAVSI
Mouse Bv8       MGDPRCAPLLLLLLPPLLFTPRAGDAAVITGACDKDSQCGGGMCCAVSI

                60        70        80        90        100
Human BV8       WVKSIRICTPMGKLGDSCHPLTRKNNTGNGRQERRKRRSKRKKEVPFF-G
Mouse Bv8       WVKSIRICTPMGQVGDSCHPLTRKSHVANGRQERRRAKRRKRKKEVVPFWG

                110       120       129
Human BV8       RRMHHTCPCLPGLACLRTSFNRFICLAQK
Mouse Bv8       RRMHHTCPCLPGLACLRTSFNRFICLARK
```

FIGURE 7

```
1    tggcctcccc agcttgccag gcacaaggct gagcgggagg aagcgagagg catctaagca ggcagtgttt
71   tgccttcacc ccaagtgacc atgagaggtg ccacgcgagt ctcaatcatg ctcctcctag taactgtgtc
141  tgactgtgct gtgatcacag gggcctgtga gcgggatgtc cagtgtgggg caggcacctg ctgtgccatc
211  agcctgtggc ttcgagggct gcggatgtgc accccgctgg ggcgggaagg cgaggagtgc caccccggca
281  gccacaaggt ccccttcttc aggaaacgca agcaccacac ctgtccttgc ttgcccaacc tgctgtgctc
351  caggttcccg gacggcaggt accgctgctc catggacttg aagaacatca atttttaggc gcttgcctgg
421  tctcaggata cccaccatcc ttttcctgag cacagcctgg atttttattt ctgccatgaa acccagctcc
491  catgactctc ccagtcccta cactgactac cctgatctct cttgtctagt acgcacatat gcacacaggc
561  agacatacct cccatcatga catggtcccc aggctggcct gaggatgtca cagcttgagg ctgtggtgtg
631  aaaggtggcc agcctggttc tcttccctgc tcaggctgcc agagaggtgg taaatggcag aaaggacatt
701  ccccctcccc tccccaggtg acctgctctc tttcctgggc cctgcccctc tccccacatg tatccctcgg
771  tctgaattag acattcctgg gcacaggctc ttgggtgcat tgctcagagt cccaggtcct ggcctgaccc
841  tcaggccctt cacgtgaggt ctgtgaggac caatttgtgg gtagttcatc ttccctcgat tggttaactc
911  cttagtttca gaccacagac tcaagattgg ctcttcccag agggcagcag acagtcaccc caaggcaggt
981  gtagggagcc cagggaggcc aatcagcccc ctgaagactc tggtcccagt cagcctgtgg cttgtggcct
1051 gtgacctgtg accttctgcc agaattgtca tgcctctgag gccccctctt accacacttt accagttaac
1121 cactgaagcc cccaattccc acagcttttc cattaaaatg caaatggtgg tggttcaatc taatctgata
1191 ttgacatatt agaaggcaat tagggtgttt ccttaaacaa ctcctttcca aggatcagcc ctgagagcag
1261 gttggtgact ttgaggaggg cagtcctctg tccagattgg ggtgggagca agggacaggg agcagggcag
1331 gggctgaaag gggcactgat tcagaccagg gaggcaacta cacaccaaca tgctggcttt agaataaaag
1401 caccaactga aaaaa.
```

FIGURE 8

```
                                                    10
Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val Ser
        20                                              30
Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala
                    40                                          50
Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr
                                60
Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val Pro
    70                                          80
Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu Leu
                90                                      100
Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu Lys Asn
        105
Ile Asn Phe
```

Figure 9

```
1    GAA GTG AGG GGT ACC AAA GTA GAC TGT GTT TGT CGT CAC CTC AAG TGA TC

51   ATG AGA GGC GCT GTG CAT ATC TTC ATC ATG CTC CTT CTA GCA ACG GCG TCC
     M   R   G   A   V   H   I   F   I   M   L   L   L   A   T   A   S

102  GAC TGT GCG GTC ATC ACA GGG GCC TGT GAA CGA GAT ATC CAG TGT GGG GCC
     D   C   A   V   I   T   G   A   C   E   R   D   I   Q   C   G   A

153  GGC ACC TGC TGC GCT ATC AGT CTG TGG CTG CGG GGC CTG CGG TTG TGT ACC
     G   T   C   C   A   I   S   L   W   L   R   G   L   R   L   C   T

204  CCA CTG GGG CGT GAA GGA GAG GAG TGC CAC CCA GGA AGC CAC AAG ATC CCC
     P   L   G   R   E   G   E   E   C   H   P   G   S   H   K   I   P

255  TTC TTG AGG AAA CGC CAA CAC CAT ACC TGT CCC TGC TCA CCC AGC CTG CTG
     F   L   R   K   R   Q   H   H   T   C   P   C   S   P   S   L   L

306  TGC TCC AGG TTC CCG GAC GGC AGG TAC CGC TGC TTC CGG GAC TTG AAG AAT
     C   S   R   F   P   D   G   R   Y   R   C   F   R   D   L   K   N

357  GCC AAC TTT TAGTTTGTCTGGACTCTGTCTGGAGCCTGACTGGGTGACCTCTTGCTTTACACCT
     A   N   F   *

     GTGTGATTTAGCTCCCTGCAACTTCGCCATTCCCCATCTTGTCCGTGTATGTGCAGACAGGCAGACC
     TTCCGCTATGGAATAGTTCACCAGGGTGCAGAGAGGAGTTCGTGGCCTTGAGAAGTTGGCCAGCCCG
     ACCTTCCTGGCTCAGACTGCCTGAAGTTGTGACAGTGTGGGCCTTCTCAGTTGCCTGCCCCTTCCTG
     CATGTGCGCTTCTTCCTAAACCACACCTTTCTGGGCACTGGCCCATGGATGCACCACTAAATCAACA
     GGTCTGTGGGGTGGATGATCAACTTTCTCTCCATTTTTCTTTTATTGACTGGCTTCCTAATTTAAGG
     ACTGT
```

Figure 10

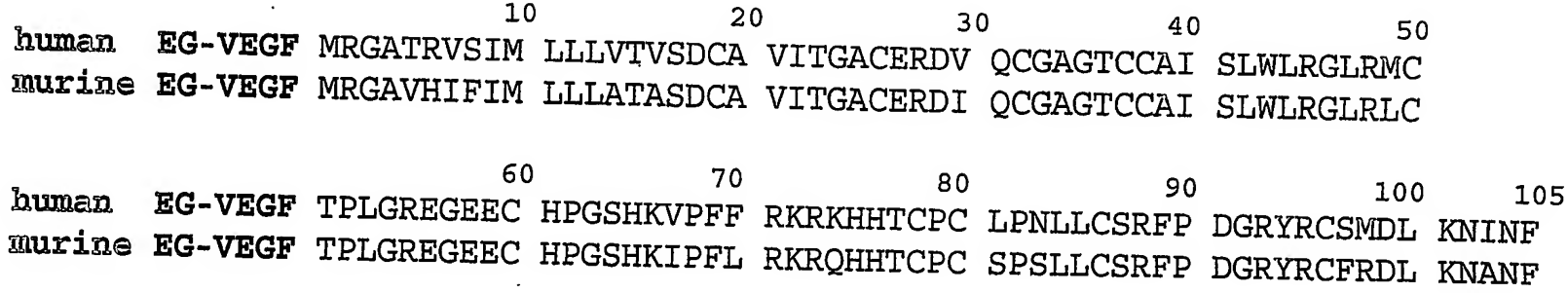

10 20 30 40 50
human EG-VEGF MRGATRVSIM LLLVTVSDCA VITGACERDV QCGAGTCCAI SLWLRGLRMC
murine EG-VEGF MRGAVHIFIM LLLATASDCA VITGACERDI QCGAGTCCAI SLWLRGLRLC
60 70 80 90 100 105
human EG-VEGF TPLGREGEEC HPGSHKVPFF RKRKHHTCPC LPNLLCSRFP DGRYRCSMDL KNINF
murine EG-VEGF TPLGREGEEC HPGSHKIPFL RKRQHHTCPC SPSLLCSRFP DGRYRCFRDL KNANF

Figure 11

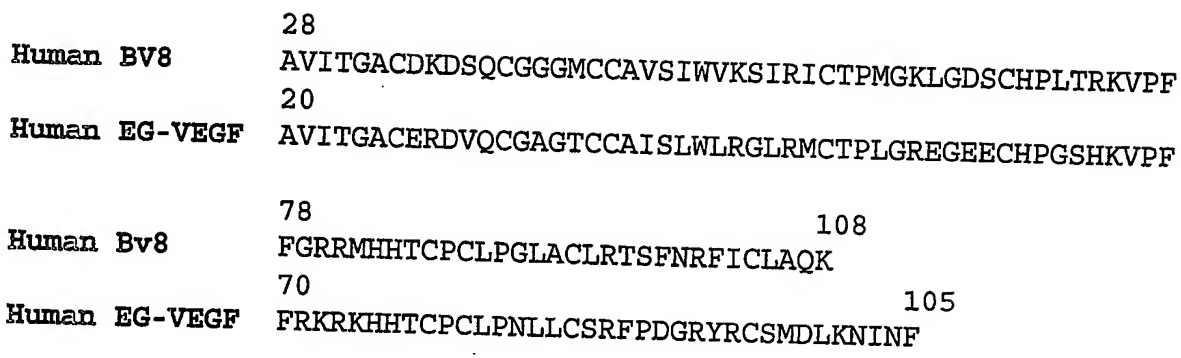

28
Human BV8
AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPF
20
Human EG-VEGF
AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPF
78
108
Human Bv8
FGRRMHHTCPCLPGLACLRTSFNRFICLAQK
70
105
Human EG-VEGF
FRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

FIGURE 12

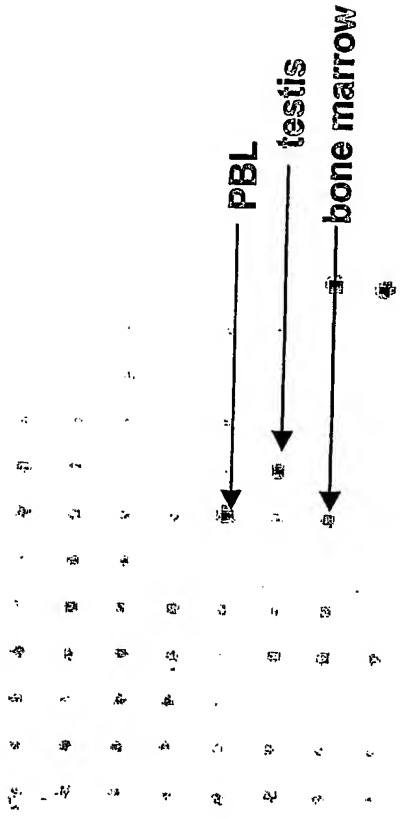


FIGURE 13

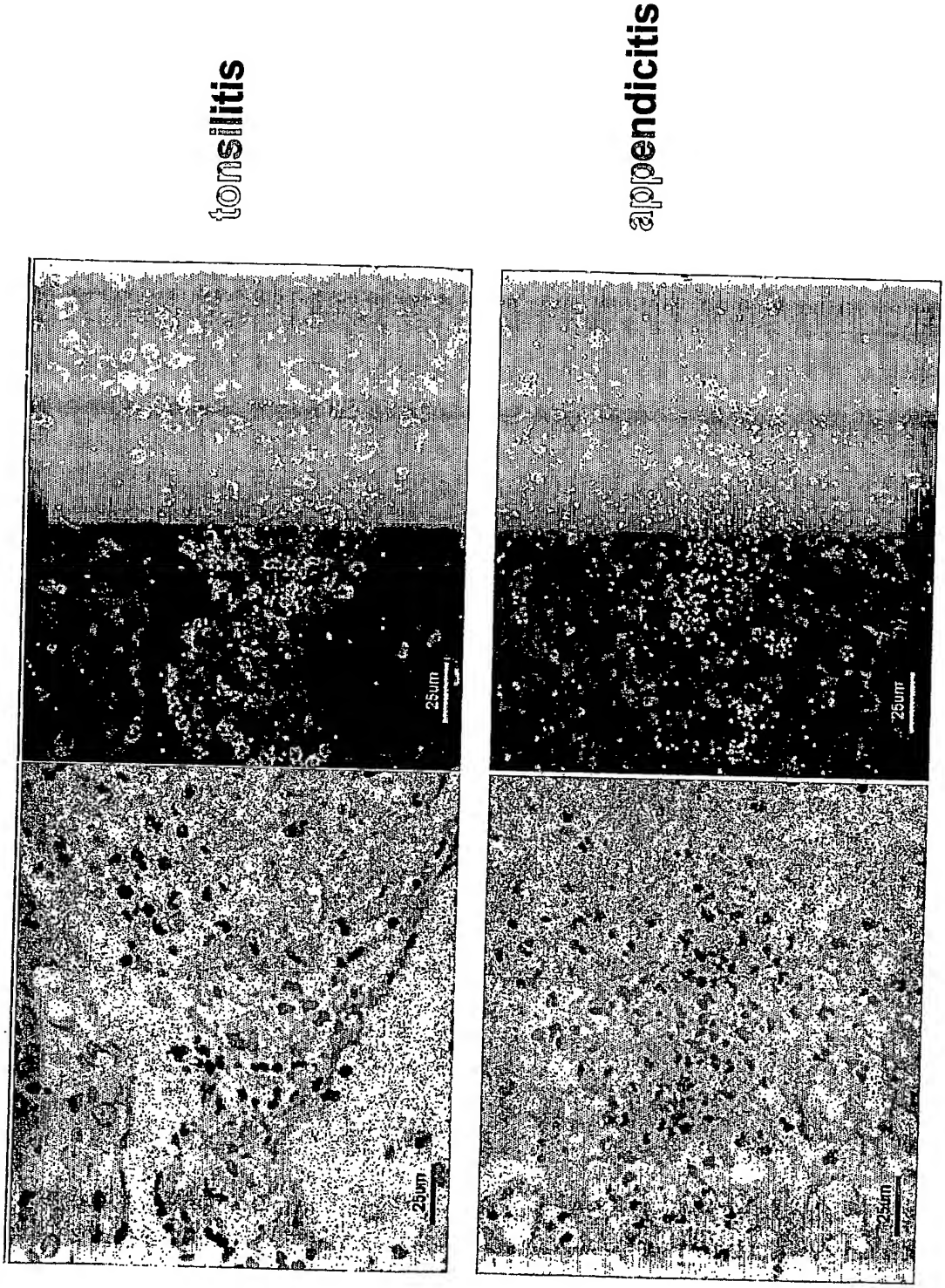
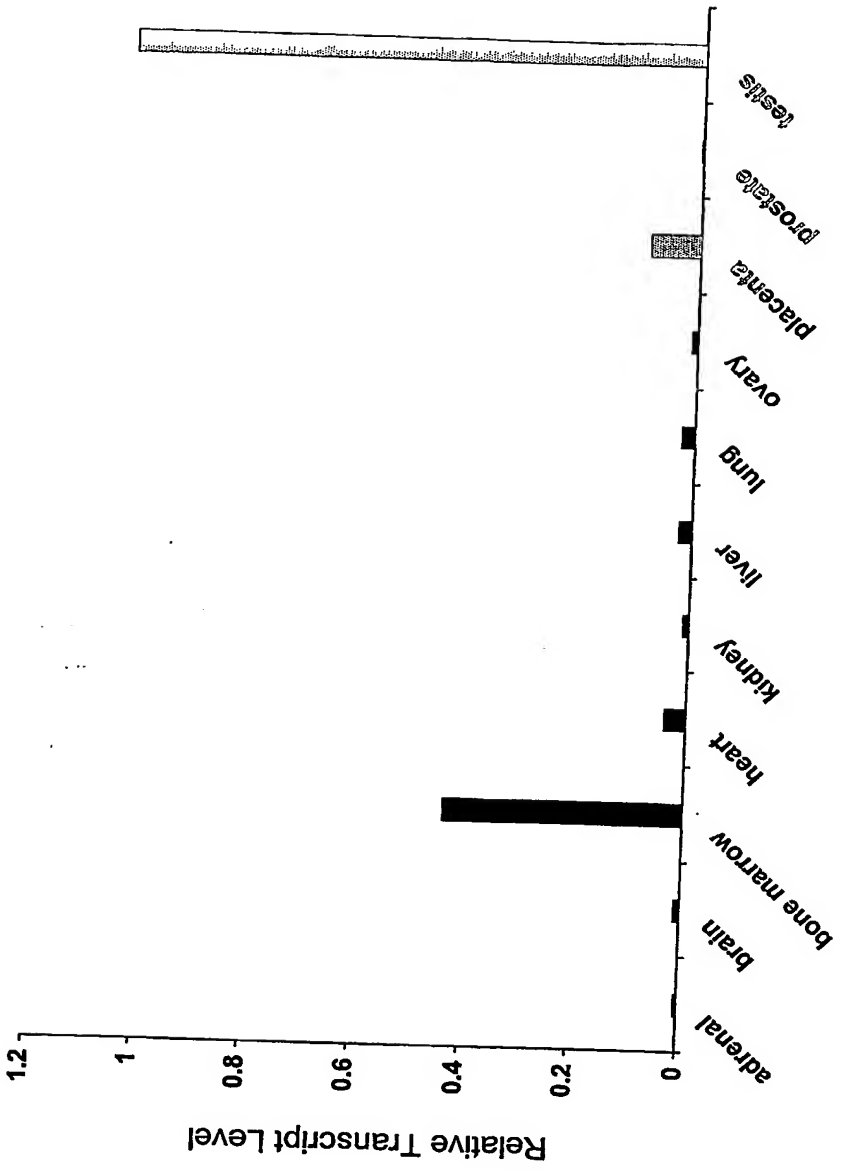


FIGURE 14


Relative Transcript Level
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1
0.8
0.6
0.4
0.2
0
adrenal
brain
bone marrow
heart
kidney
liver
lung
ovary
placenta
prostate
testis

FIGURE 15A

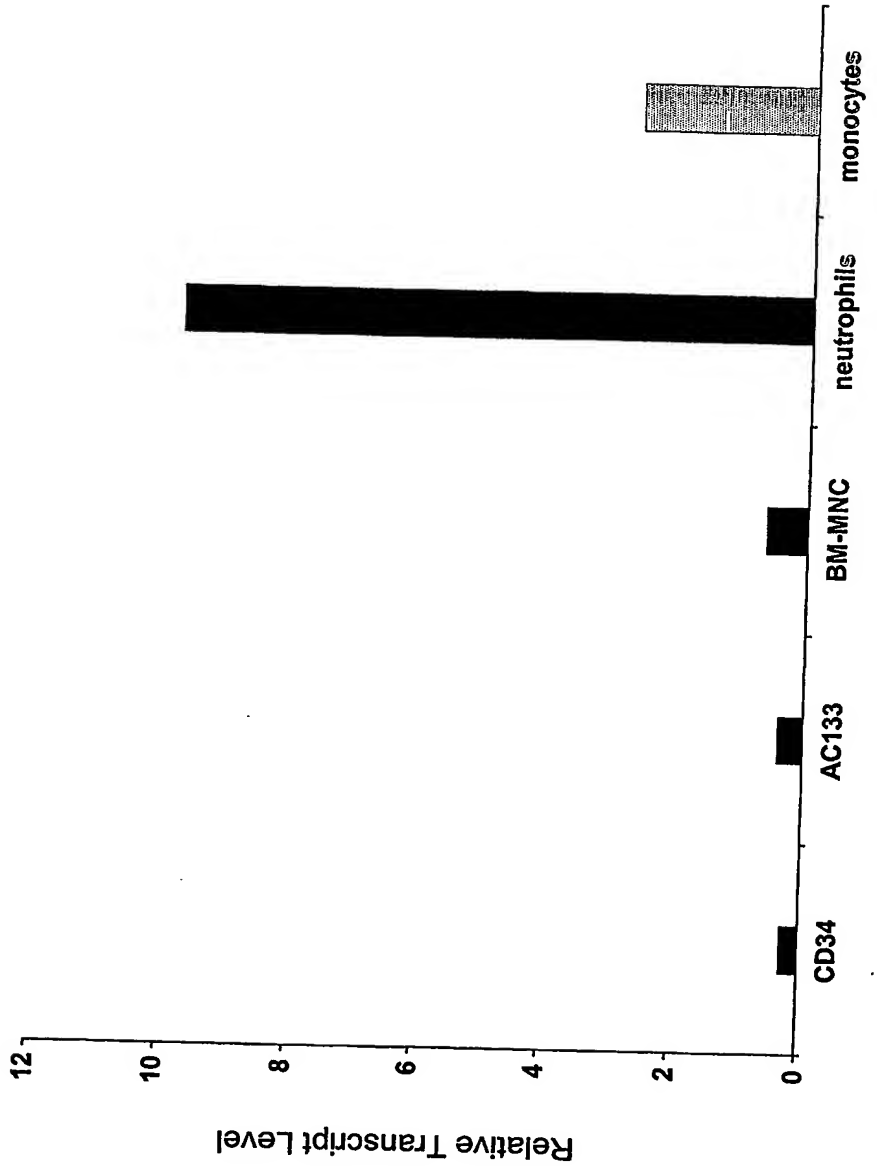

Relative Transcript Level
0
2
4
6
8
10
12
CD34
AC133
BM-MNC
neutrophils
monocytes

FIGURE 15B

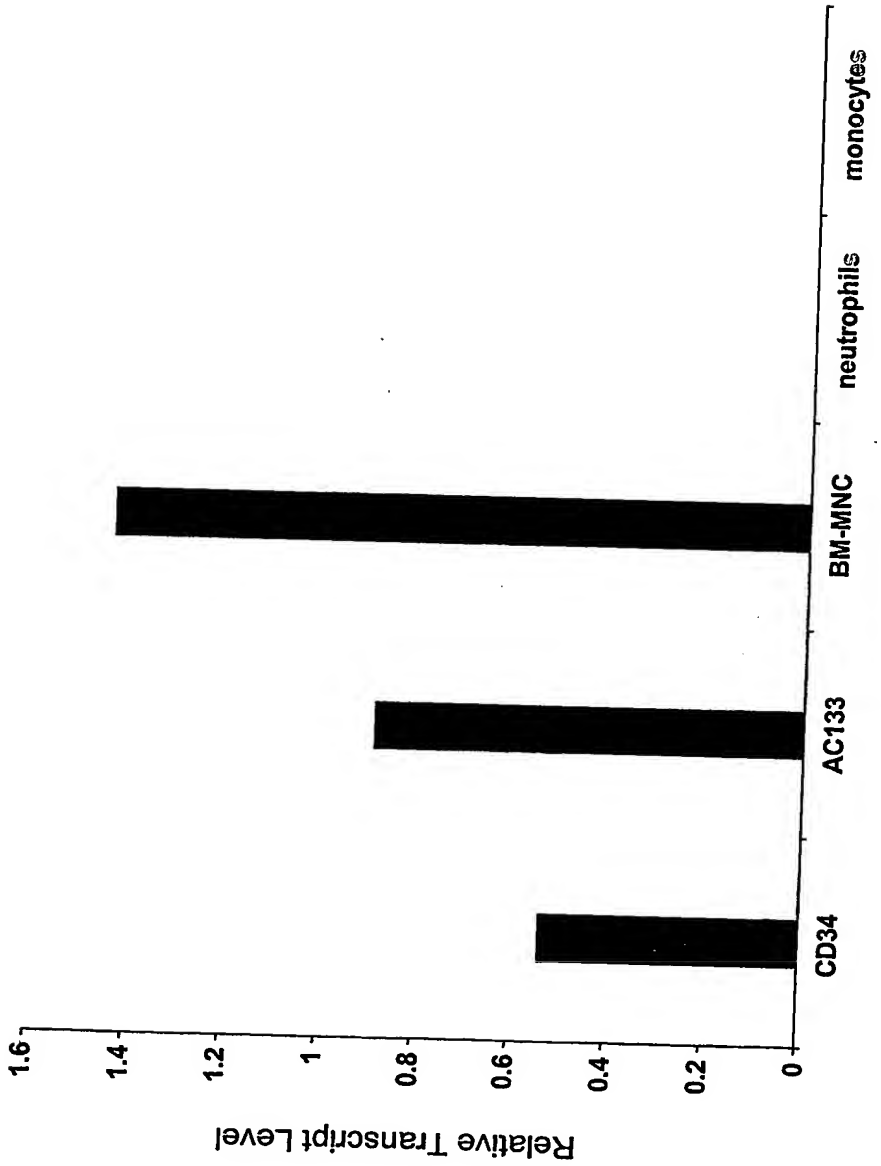

Relative Transcript Level
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
CD34
AC133
BM-MNC
neutrophils
monocytes

FIGURE 15C

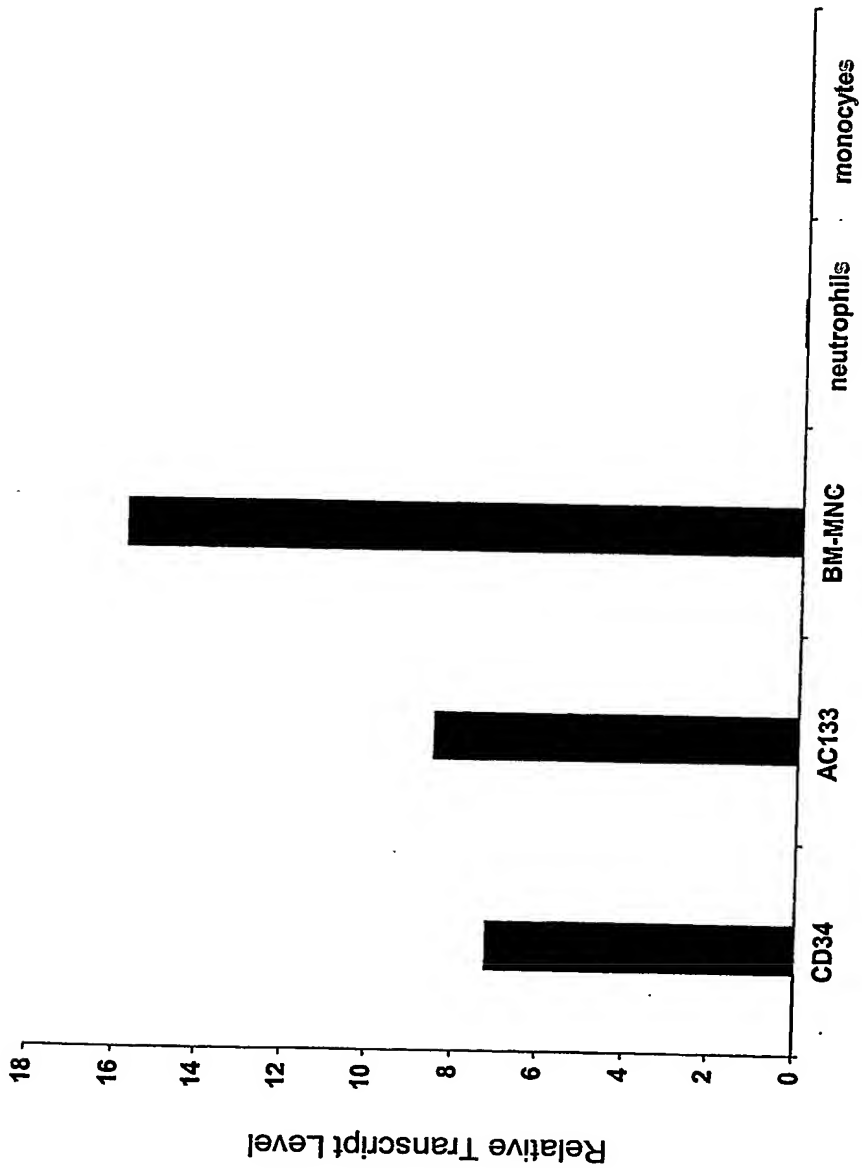
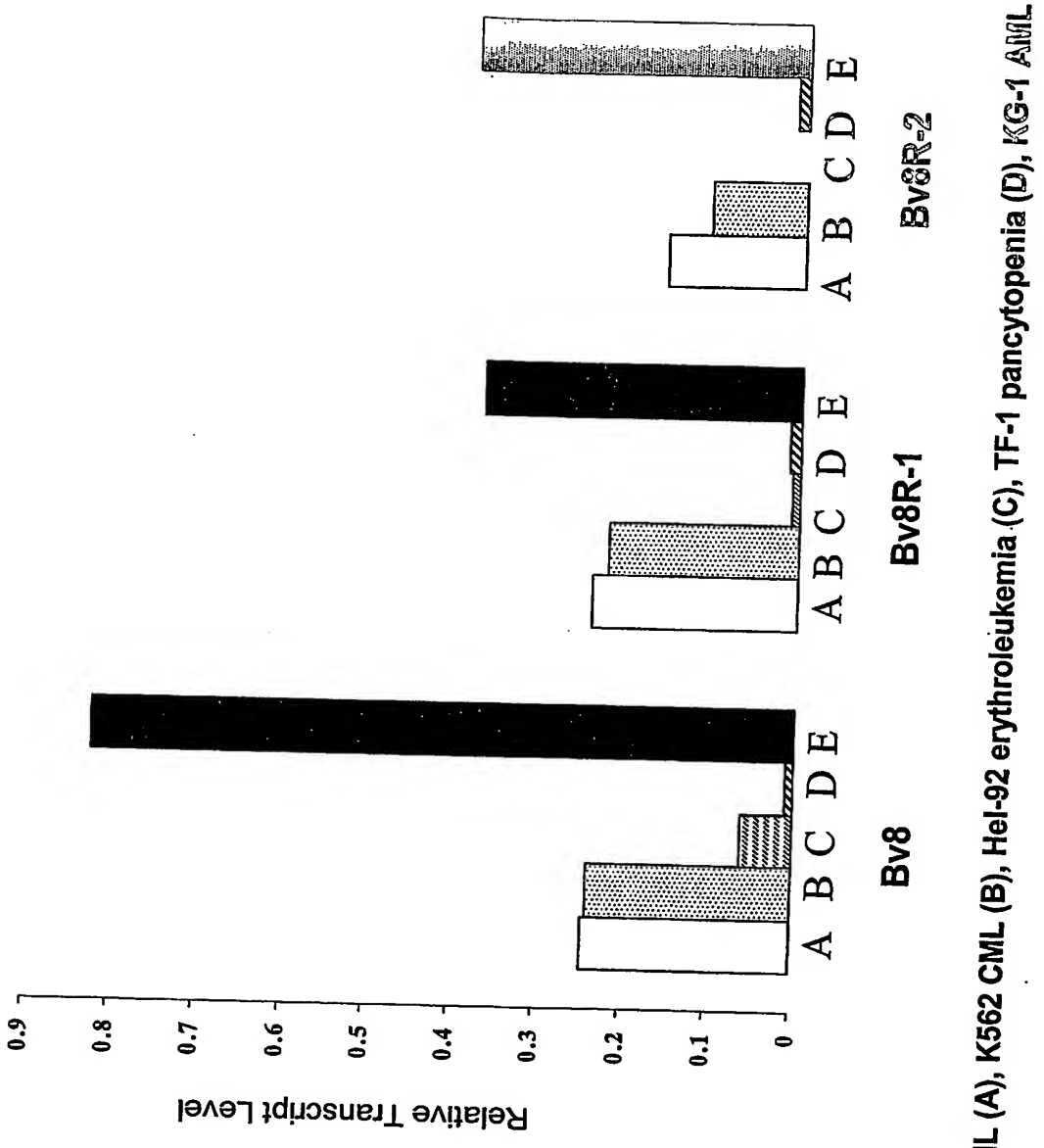

Relative Transcript Level
0
2
4
6
8
10
12
14
16
18
CD34
AC133
BM-MNC
neutrophils
monocytes

FIGURE 15D



HL60 CML (A), K562 CML (B), Hel-92 erythroleukemia (C), TF-1 pancytopenia (D), KG-1 AML (E)

FIGURE 16

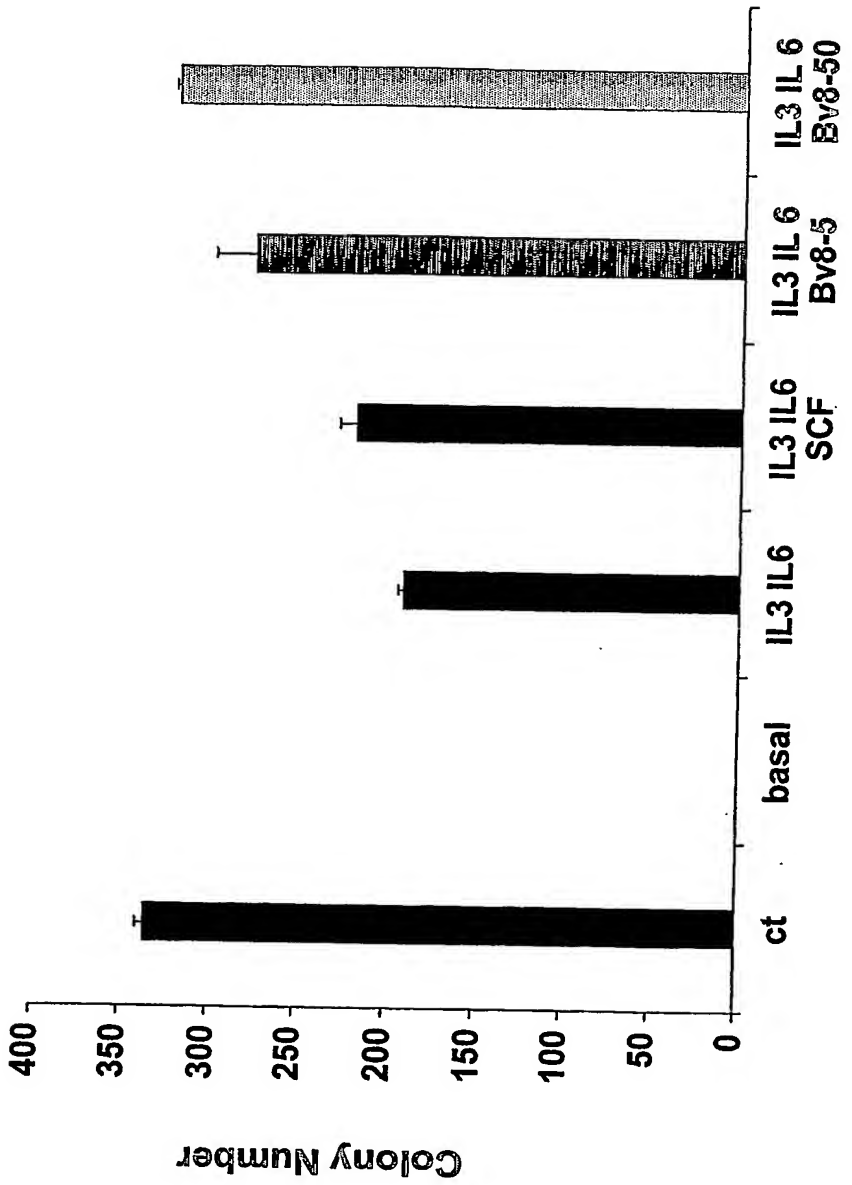

Colony Number
400
350
300
250
200
150
100
50
0
ct
basal
IL3 IL6
IL3 IL6 SCF
IL3 IL 6 Bv8-5
IL3 IL 6 Bv8-50

FIGURE 17A

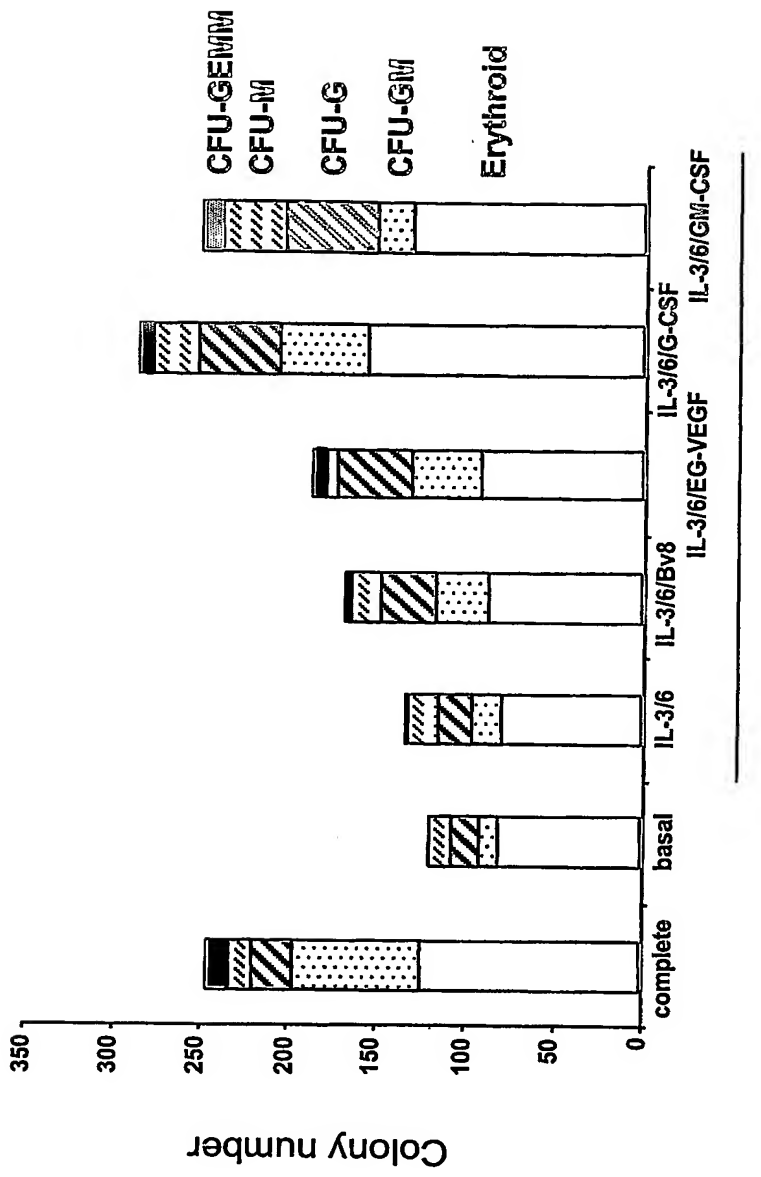

CFU-GEMM
CFU-M
CFU-G
CFU-GM
Erythroid
Colony number
350
300
250
200
150
100
50
0
complete
basal
IL-3/6
IL-3/6/Bv8
IL-3/6/EG-VEGF
IL-3/6/G-CSF
IL-3/6/GM-CSF
basal

FIGURE 17B

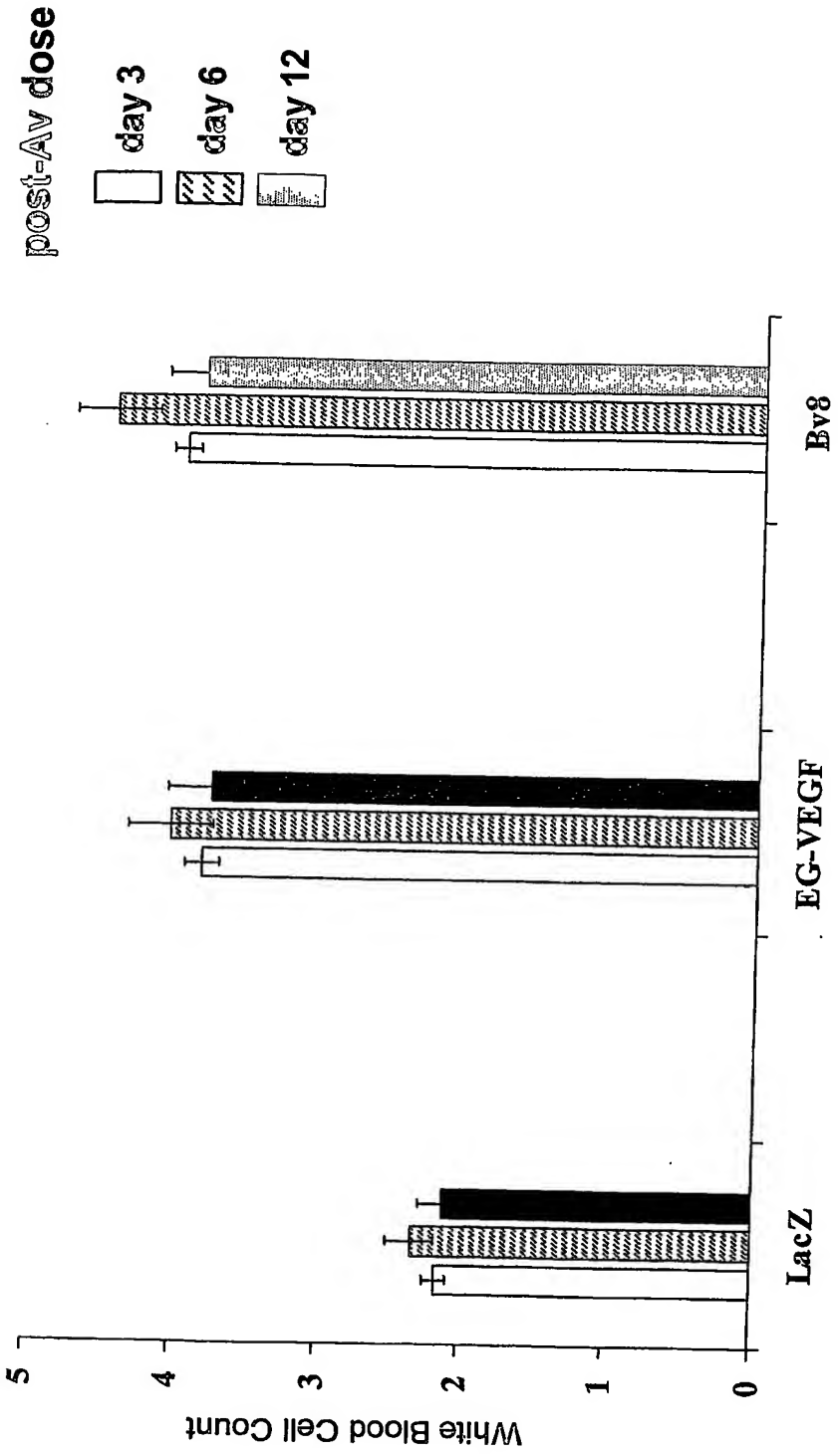

post-Av dose
day 3
day 6
day 12
White Blood Cell Count
0
1
2
3
4
5
LacZ
EG-VEGF
Bv8

FIGURE 18

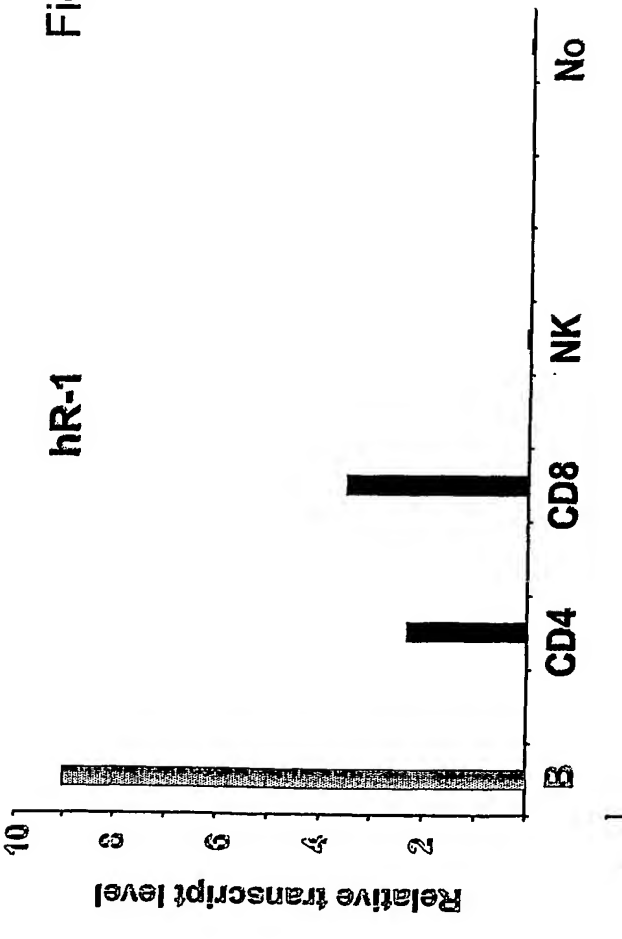


Figure 19A

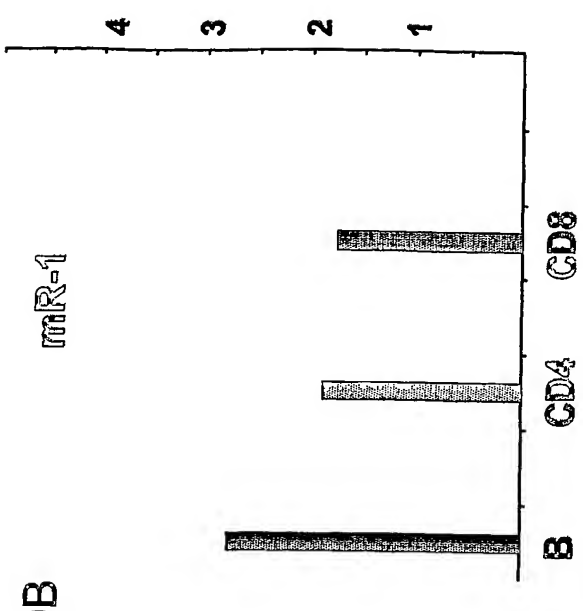


Figure 19B

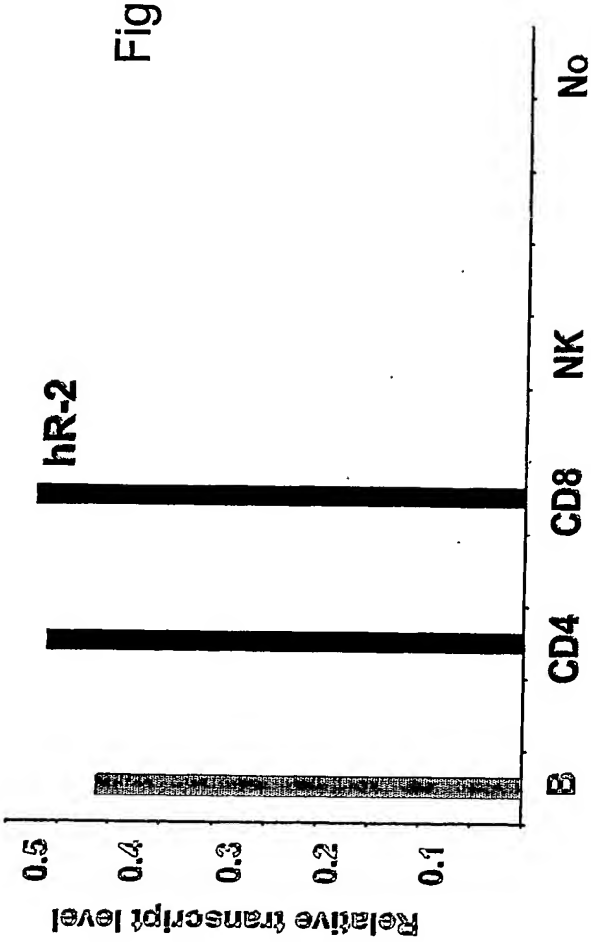


Figure 19C

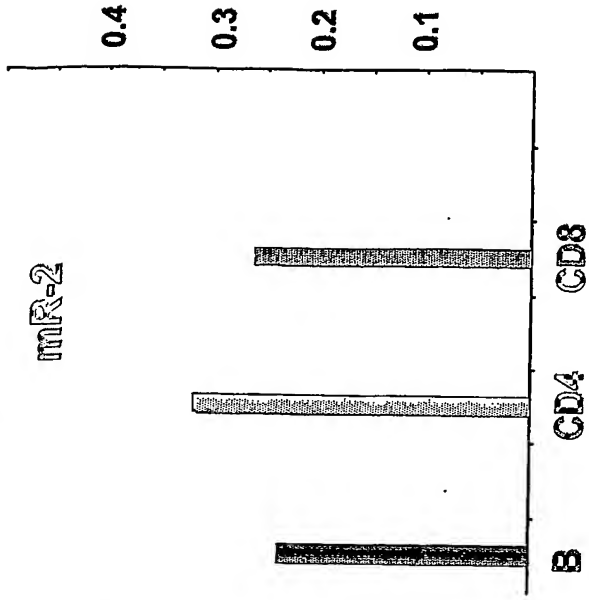


Figure 19D

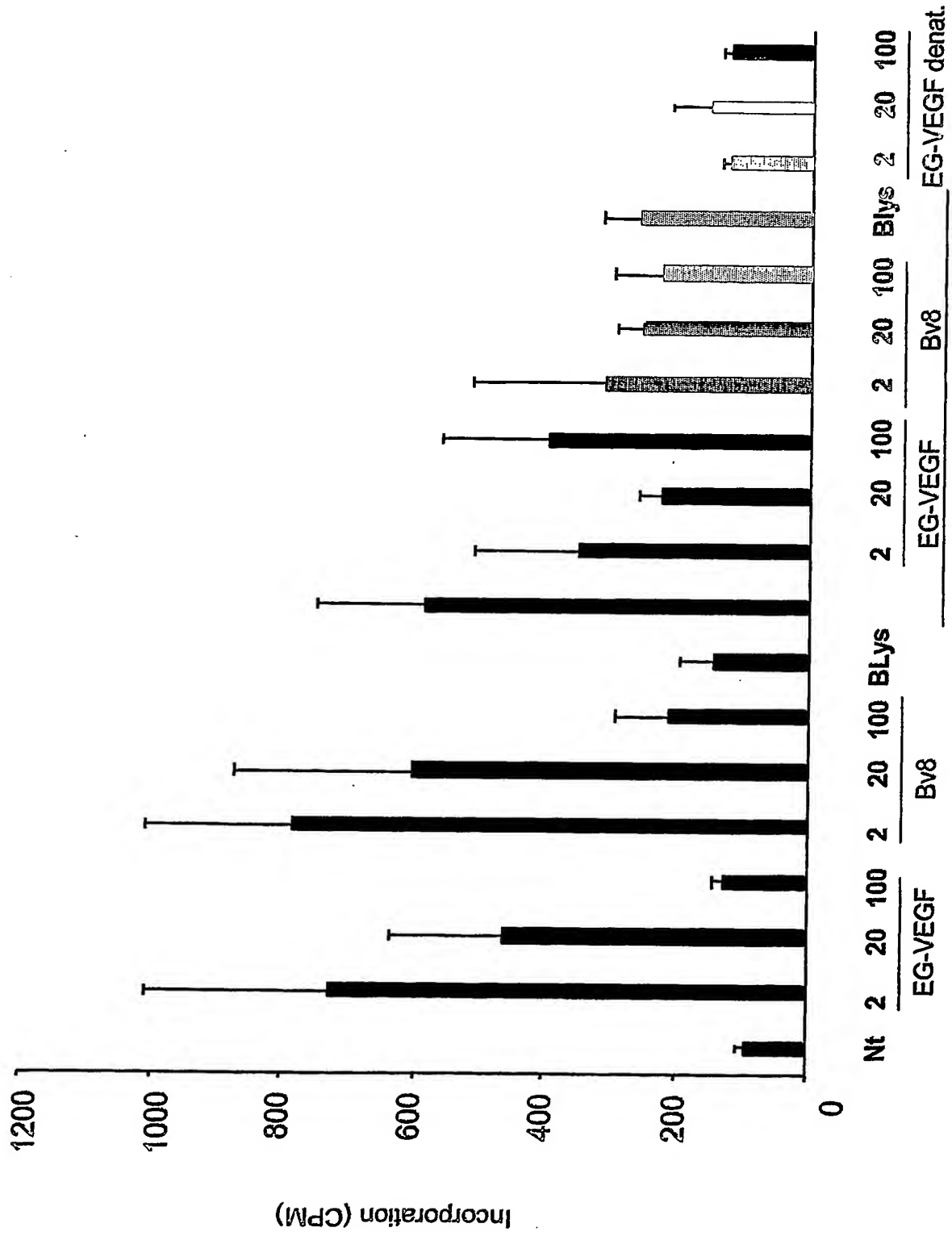


Figure 20 + α-IgM

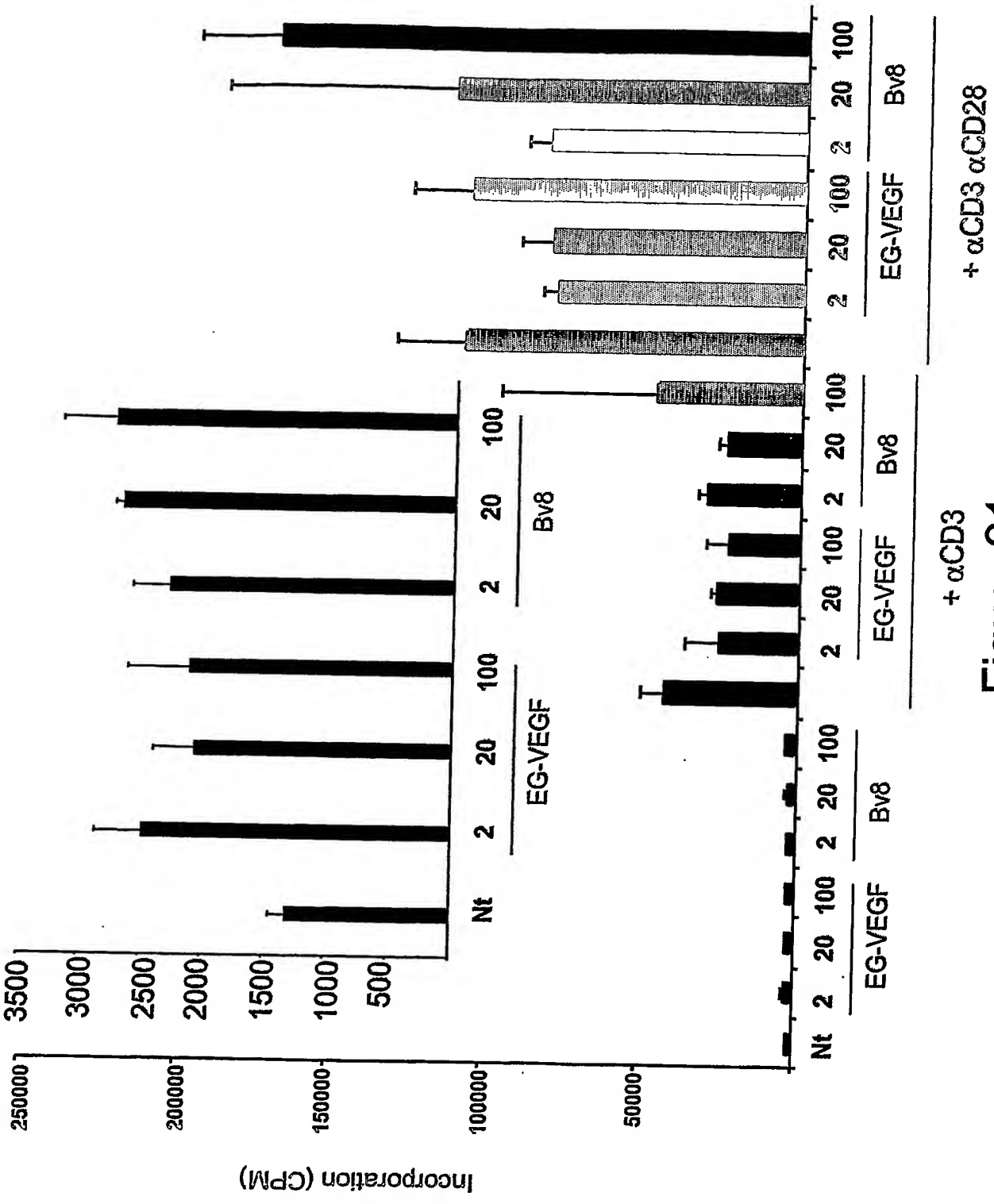

Incorporation (CPM)
250000
200000
150000
100000
50000
3500
3000
2500
2000
1500
1000
500
Nt
2
20
100
EG-VEGF
Bv8
+ αCD3
+ αCD3 αCD28

Figure 21

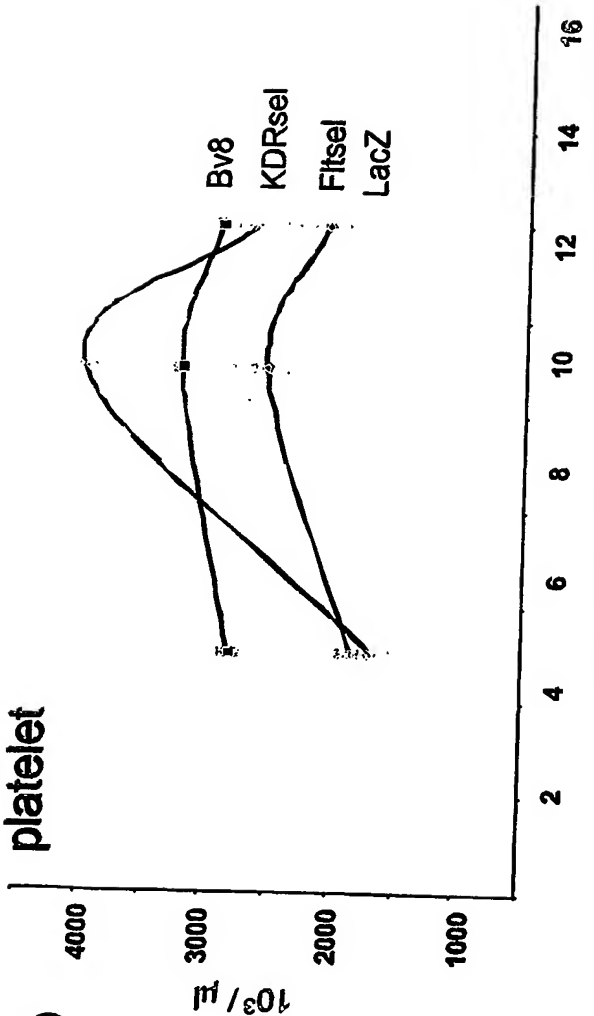


Figure 23D

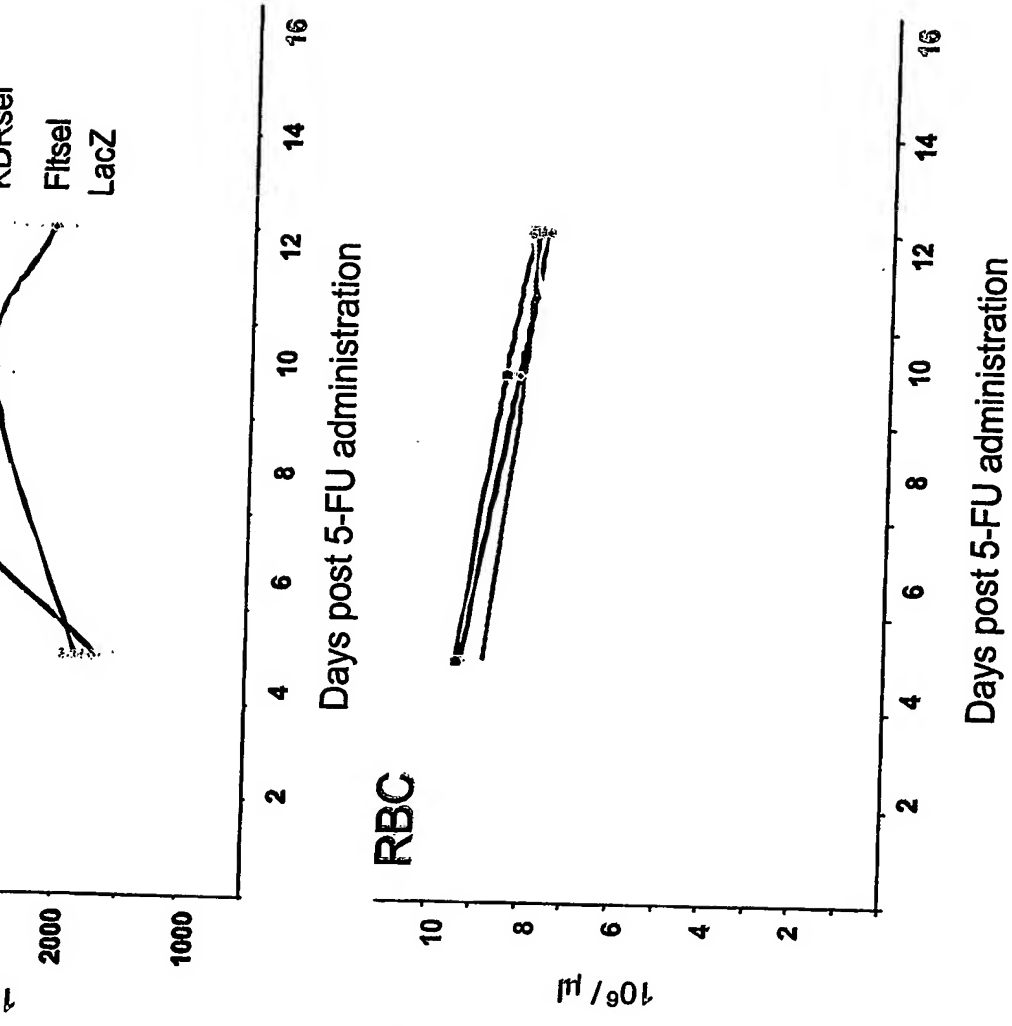


Figure 23E

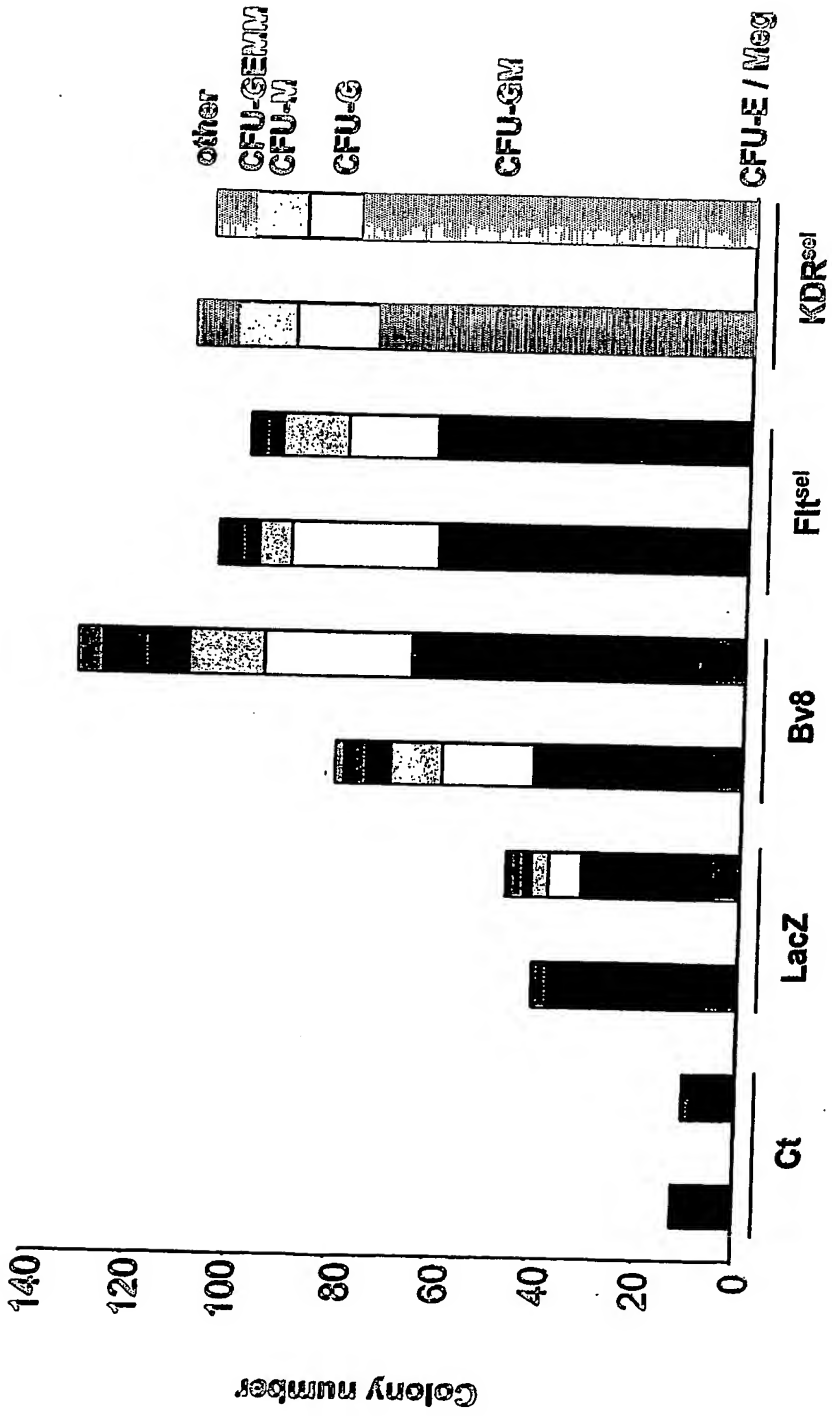

Colony number
140
120
100
80
60
40
20
0
Ct
LacZ
Bv8
Flt^{sel}
KDR^{sel}
CFU-E / Meg
CFU-GM
CFU-G
CFU-M
CFU-GEMM
other

Figure 24